

# FIGURE 1A-1

1 M A L R R S M G R P G L P P L P L P P P R L G L L L A A L A S  
 1 CCGCCGATGG CGCTAGGCG GAGCATGGG CGGCCGGGC TCCGCCGCT GCGCTGGC CGCCACCG GGTCTGGCT GCTCTGGCTT  
 33 L L L P E S A A A G L K L M G A P V K L T V S Q G Q P V K L N C S  
 101 CTCTGCTGCT CCGGAGTCC GCGCCGCGAG GTCTGAAGCT CATGGGAGCC CCGGTGAAGC TGACAGTGC TCAGGGGCG CCGGTGAAGC TCAACTGCAG  
 66 V E G M E E P D I Q W V K D G A V V Q N L D Q L Y I P V S E Q H W  
 201 TGTGGAGGG ATGGAGGAG CTGACATCCA GTGGGTGAAG GATGGGGCTG TGGTCCAGAA CTTGGACCAG TTGTACATCC CAGTCAGCGA GCAGCACTGG  
 99 I G F L S L K S V E R S D A G R Y W C Q V E D G G E T E I S Q P V W  
 301 ATCGGCTTCC TCAGCCTGAA GTCAGTGGAG CGCTCTGAG CCGGCCGGTA CTGGTGGCAG GTGGAGGATG GGGGTGAAC CGAGATCTCC CAGCCAGTGT  
 133 L T V E G V P F F T V E P K D L A V P P N A P F Q L S C E A V G P  
 401 GGCTCAGGT AGAAGTGTG CCATTTTCA CAGTGGAGCC AAAGATCTG GCAGTGGCC CCAATGCCCC TTCCAACTG TCTTGTGAGG CTGTGGGTCC  
 166 P E P V T I V W W R G T T K I G G P A P S P S V L N V T G V T Q S  
 501 CCTGAACCT GTTACCATTG TCTGGTGGAG AGGAACCTAG AAGATCGGG GACCCGCTCC CTCTCCATCT GTTTAAATG TAACAGGSGT GACCCAGAGC  
 199 T M F S C E A H N L K G L A S S R T A T V H L Q A L P A A P A A P F N I T  
 601 ACCATGTTTT CCTGTGAAGC TCAACAACCTA AAAGGCCCTG CCTCTTCTG CACAGCCACT GTTACCTTC AAGCACTGCC TGCAGCCCCC TTCAACATCA  
 233 V T K L S S S N A S V A W M P G A D G R A L L Q S C T V Q V T Q A  
 701 CCGTGACAA GCTTCCAGC AGCAACGCTA GTGTGGCCTG GATGCCAGT GCTGATGGC GAGCTCTGCT ACAGTCTGT ACAGTTCAGG TGACACAGGC  
 266 P G G W E V L A V V V P V P P F T C L L R D L V P A T N Y S L R V  
 801 CCCAGGAGC TGGGAAGTCC TGGCTGTTGT GGTCCCTGTG CCCCCCTTA CTGCTGCTG CCGGACCTG GTGCCCTGCC CCAACTACAG CCTCAGGSGT  
 299 R C A N A L G P S P Y A D W V P F Q T K G L A P A S A P Q N L H A I  
 901 CGCTGTGCA ATGCTTGGG GCGCTCTCC TATGCTGACT GGTGCGCTT TCAGACCAAG GGTCTAGCCC CAGCCAGCGC TCCCCAAAC CTCCATGCCA  
 333 R T D S G L I L E W E E V I P E A P L E G P L G P Y K L S W V Q D  
 1001 TCCGCACAGA TTCAGGCCTC ATCTTGGAGT GGAAGNAAGT GATCCCCGAG GCGCTTTGG AAGGCCCTT GGGACCTAC AAAGTGTCT GGTTCAGA  
 366 N G T Q D E L T V E G T R A N L T G W D P Q K D L I V R V C V S N  
 1101 CAATGGAAC CAGGATGAG TGACAGTGA GGGGACAGG GCAATTGA CAGGCTGGGA TCCCCAAAG GACCTGATG TACGTGTG CGTCTCCAAT  
 399 A V G C G P W S Q P L V V S S H D R A G Q Q G P P H S R T S W V P V  
 1201 GCAGTTGGCT GTGGACCCCTG GAGTCAGCCA CTGGTGGTCT CTCTCATGA CCGTGAGGC CAGCAGGSC CTCCTCAG CCGCACATCC TGGGTACCTG  
 433 V L G V L T A L V T A A A L A L I L L R K R R K E T R F G Q A F D  
 1301 TGGTCTTGG TGTGCTAACG GCGCTGCTG CCGTGGCCTC ATCTGCTTC GAAAGAGAGC GAAAGAGAGC CGTTTGGGC AAGCCTTGA

466 S V M A R G E P A V H F R A A R S F N R E R P E R I E A T L D S L  
1401 CAGTGTCTG GCCCGGGAG AGCCAGCGT TCACTTCCGG GCAGCCCGT CCTTCAATCG AGAAGGCC GAGCGCATCG AGCCACATT GGACAGCTTG  
499 G I S D E L K E K L E D V L I P E Q Q F T L G R M L G K G E F G S V  
1501 GGCATCAGCG ATGAATAA GGAATACTG GAGGATGTGC TCATCCAGA GCAGCAGTTC ACCCTGGGCC GGATGTTGG CANAGGAGAG TTTGGTTGAG  
533 R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E F  
1601 TGCGGAGGC CCAGCTGAAG CAAGAGGATG GCTCCTTTGT GAAAGTGCT GTGAGATGC TGAAGCTGA CATCATTTGCC TCAAGCGACA TTGAAGAGTT  
566 L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I  
1701 CCTCAGGAA GCAGCTTGA TGAAGGAGTT TGACCATCCA CACGTGGCCA AACTTGTGG GGTAAAGCCTC CGGAGCAGG CTAAGGCGG TCCTCCCATC  
599 P M V I L P F M K H G D L H A F L L A S R I G E N P F N L P L Q T L  
1801 CCCATGCTCA TCTTGCCCTT CATGAAGCAT GGGGACCTGC ATGCCCTTCT GCTCGCCTCC CGGATGCGG AGAACCCCTT TAACCTACCC CTCACAGCCC  
633 I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A E  
1901 TGATCCGCTT CATGTTGAC ATTGCTTCCG GCATGGAGTA CCTGAGCTCT CGGAATCTCA TCCACCGAGA CCTGGCTGCT CGGAATTGCA TGCTGGCAGA  
666 D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L P V K W  
2001 GGACATGACA GTGTGTGTGG CTGACTTCCG ACTCTCCCG AGATCTACA GTGGGACTA CTATCGTCAA GGCTGTGCCT CCNAAGTCC TGTCNAAGTGG  
699 L A L E S L A D N L Y T V Q S D V W A F G V T M W E I M T R G Q T P  
2101 CTGGCCCTGG AGAGCCTGCC CGACAACCTG TATACTGTGC AGAGTGACGT GTGGCGTTC GGGGTGACCA TGTGGGAGAT CATGACACGT GGGCAGACGC  
733 Y A G I E N A E I Y N Y L I G G N R L K Q P P E C M E D V Y D L M  
2201 CATATGCTGG CATCGAAAC GCTGAGATT ACAACTACCT CATTTGGCGG AACCGCCTGA AACAGCCTCC GAGTGTATG GAGGACGTGT ATGATCTCAT  
766 Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A  
2301 GTACCACTGC TGGAGTGTG ACCCCAAGCA GCGCCCGAGC TTTACTTGTG TCGGAATGGA ACTGGAGAAC ATCTTGGGCC AGCTGTCTGT GCTATCTGCC  
799 S Q D P L Y I N I E R A E E P T A G G S L E L P G R D Q P Y S G A G  
2401 AGCCAGGACC CCTTATACAT CAACATCAG AGAGCTGAG AGCCCACTGC GGGAGGCAGC CTGGAGCTAC TCAGCCCTAC AGTGGGGCTG  
833 D G S G M G A V G G T P S D C R Y I L T P G G L A E Q P G Q A E H  
2501 GGGATGGCAG TGGCATGGG GCAGTGGGTG GCACTCCCG TACTGTGCG TACATACTCA CCCCCGAGG GCTGGCTGAG CAGCCAGGCG AGGCAGAGCA  
866 Q P E S P L N E T Q R L L L L Q Q G L L P H S S C O  
2601 CCAGCCAGAG AGTCCCTTCA ATGAGACACA GAGGCTTTTG CTGCTGCAGC AAGGGCTACT GCCACACAGT AGCTGTTAGC CCACAGGCAG AGGGCATCGG  
2701 GGCCATTGG CCGGCTCTG TGGCCACTGA GCTGGCTGAC TAAGCCCCGT CTGACCCCG AGGTGTGGA GGCTCTGTG GTAGTCTCTC  
2801 CAAGCTGTG TGGGAAGCCC GGAATGACCA ATCACCACA TCCAGTTCT TCCTGCAACC ACTCTGTGCC CAGCCTGGCA TCAGTTTAGG CCTTGGCTTG

FIGURE 1A-3

2901 ATGGAAGTGG GCCAGTCCCTG GTTGCTCTGAA CCCAGGCAGC TGGCAGGAGT GGGGTGGTTA TGTTTCCATG GTTACCATGG GTGTGGATGG CAGTCTGGGG  
3001 AGGGCAGGTC CAGCTCTGTG GGCCCTACCC TCCTGCTGAG CTGCCCCCTGC TGCTTAAAGT CATGCATTGA GCTGCCCTCCA GCCTGGTGGC CCAGCTATTA  
3101 CCACACTTGG GGTTTAAATA TCCAGGTGTG CCCCTCCAAG TCACAAAGAG ATGTCCCTTGT AATATTCCCT TTTAGGTGAG GGTGGTAAG GGGTTGGTAT  
3201 CTCAGGTCTG AATCTTCACC ATCTTTCTGA TTCCGCACCC TGCCTACGCC AGGAGAAGTT GAGGGGAGCA TGCTTCCCTG CAGCTGACCG GGTACACAAA  
3301 AGGCATGCTG GAGTACCCAG CCTATCAGGT GCCCCCTCTC CAAAGGCAGC GTGCCGAGCC AGCAAGAGGA AGGGGTGCTG TGAGGCTTGC CCAGGAGCAA  
3401 GTGAGGCCGG AGAGGAGTTC AGGAACCCTT CTCCATACCC ACAATCTGAG CACGCTACCA AATCTCAANA TATCCTAAGA CTAACAAAGG CAGCTGTGTC  
3501 TGAGCCCCAAC CCTTCTAAAC GGTGACCCTT AGTGCCCACT TCCCCCTCTAA CTGGACAGCC TCTTCTGTCC CAAGTCTCCA GAGAGAAATC AGGCCTGATG  
3601 AGGGGAATT C

# FIGURE 1

1 CCTCGCCAC CCTCCTCTCA GCGCTCGGG GCGGGGCGG GCATGTGCG CGTCGCCGC GATGGCGTG AGGCGGAGCA TGGGTGGCC GGGGCTCCGG

14 P L L L A G L A S L L L P G S A A A G L K L M G A P V K M T V S Q G

101 CCGCTGCTG TGGGGGACT GGCTTCTCTG CTGCTCCCG GGTCTCGGC CGCAGGCTG AGCTCATGG GCGCCCACT GAAGATGACC GTGTCTCAGG

48 Q P V K L N C S V E G M E D P D I H W M K D G T V V Q N A S Q V S

201 GGCAGCCAGT GAAGCTCAAC TGCAGCGTG AGGGATGGA GGACCTGAC ATCCACTGGA TGAAGGATGG CACCCTGGT CAGAATGCA GCCAGGTGTC

81 I S I S E H S W I G L L S L K S V E R S D A G L Y W C Q V K D G E

301 CATCTCCATC AGCAGCACA GCTGGATTGG CTTACTCAGC CTAAGTCAG TGGAGCGTG TGATCTGGC CTGACTGGT GCCAGGTGAA GGATGGGAG

114 E T K I S Q S V W L T V E G V P F F T V E P K D L A V P P N A P F Q

401 GAAACCAAGA TCTCTCAGTC AGTATGGCTC ACTGTGMA GGTGTCCATT CTTACACAGT GACCAAAAG ATCTGGCGGT GCCACCAAT GCCCTTTTC

148 L S C E A V G P P E P V T I Y W W R G L T K V G G P A P S P S V L

501 AGCTGCTTG TGAGGCTGT GGTCTCTCAG AACCGTAAC CATTACTGG TGGAGAGGAC TCACTAAGGT TGGGGACCT GCTCCCTCTC CCTCTGTTTT

181 N V T G V T Q R T E F S C E A R N I K G L A T S R P A I V R L Q A

601 AAATGTGACA GGAGTGACC AGGCACAGA GTTTTCTTGT GAAGCCCGCA ACATAAAG CCTGGCCACT TCCGACCAG CCATTGTTCG CCTTCAAGCA

214 P P A A P F N T T V T T I S S Y N A S V A W V P G A D G L A L L H S

701 CCGCTGCAG CTCCTTTCAA CACCACAGTA ACAACGATCT CCAGCTACAA CGTAGCGTG GCCTGGGTG CAGGTGCTGA CCGCTAGCT CTGCTGCATT

248 C T V Q V A H A P G E W E A L A V V V P V P P F T C L L R N L A P

801 CCTGTACTGT ACAGGTGGCA CACGCCCCAG GAGAAATGGA GGCCCTTGT GTTGTGGTTC CTGTGCCACC TTTTACCTGC CTGCTTCGA ACTTGGCCCC

281 A T N Y S L R V R C A N A L G P S P Y G D W V P F Q T K G L A P A

901 TGCCACCAAC TACAGCCTTA GGTGCGGTG TGCCAATGCC TTGGGCCCTT CTCCTACCG CGACTGGGTG CCCTTTTCA CAAAGGCGCT AGCGCCAGCC

314 R A P Q N F H A I R T D S G L I L E W E E V I P E D P G E G P L G P

1001 AGAGCTCCTC AGAATTTCCA TGCCATTGCT ACCGACTCAG GCCTTATCTT GGAATGGAA GAAGTGATTC CTGAAGACC TGGGAAGGC CCCCTAGGAC

348 Y K L S W V Q E N G T Q D E L M V E G T R A N L T D W D P Q K D L

1101 CTTATAAGCT GTCCTGGGTC CAAGAAATG GAACCCAGGA TGAGCTGATG GTGGAAGGA CCAGGCCAA TCTGACCGAC TGGGATCCCC AGAAGGACCT

381 I L R V C A S N A I G D G P W S Q P L V V S S H D H A G R Q G P P

1201 GATTTTGGGT GTGTGTCCT CCAATGCAAT TGGTGATGG CCCTGAGTC AGCCACTGCT GGTGTCTTCT CATGACCATG CAGGAGGCA GGGCCCTCCG

414 H S R T S W V P V V L G V L T A L I T A A A L A L I L L R K R R K E

1301 CACAGCCGCA CATCTGGGT GCCTGTGGTC CTGGCGGTG TCACGCCCTT GATCAGACT GCTGCTTGG CCCTCATCCT GCTTCGGAAG AGACGCAAGG

448 T R F G Q A F D S V M A R G E P A V H F R A A R S F N R E R P E R

1401 AGACGCTTT CGGCAAGCC TTGACAGTG TCATGGCCCG AGGGAGCCA GCTGTACACT TCCGGCAGC CCGATCTTTC AATCGAGAAA GGCCTGAACG

## Figure 1B-2

481 I E A T L D S L G I S D E L K E K L E D V L I P E Q Q F T L G R M  
1501 CATTGAGGCC ACATTGGATA GCTGGGCAT CAGCATGAA TTGAAGGAAA AGCTGGAGGA TGCTCTCAT CCAGAGCAGC AGTTCCACCT CGTCCGATG  
514 L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I  
1601 TTGGGCAAG GAGAGTTTGG ATCAGTGCAG GAAGCCAGC TAAAGCAGGA AGATGGCTCC TTGCTGAAAG TGGCAGTGAA GATGCTGAAA GCTGACATCA  
548 A S S D I E E F L R E A A C M K E F D H P H V A K L V G V S L R S  
1701 TTGCCTCAAG CGACATAGAA GTGTTCTCTCC GGAAGCAGC TTGCATGAAG GAGTTTGACC ATCCACACGT GGCACAGCTT GTTGGGGTGA GCCTCCGGAG  
581 R A K G R L P I P M V I L P F M K H G D L H A F L L A S R I G E N  
1801 CAGGCTAAA GGTGCTCTCC CCATTCCCAT GGTATCCTG CCCTTCATGA AACATGGAGA CTTGCACGCC TTCTGTCTCG CCTCCGAAT CGGGGAGAAC  
614 P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A  
1901 CCTTTTAACC TGCCCTGCA GACCCTGGTC CGTTTCATGG TGGACATTCG CTGTGGCAAG GAGTACCTGA GTTCCCGGA CTTTCATCCAC CGAGACCTAG  
648 A R N C M L A E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C  
2001 CAGTCGGAA TTGCATGCTG GCCAGGACA TGACAGTGTG TGTGGCTGAT TTTCGACTCT CTCGGAAT CTATAGCGGG GACTATTATC GTCAGGGCTG  
681 A S K L P V K W L A L E S L A D N L Y T V H S D V W A F G V T M W  
2101 TGCTCCCAA TTGCCGTCA AGTGGCTGGC CTGGAGAGC TTGGCTGACA ACTGTATAC TGTACACAGT GATGTGTGG CCTTCGGGGT GACCATGTGG  
714 E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K Q P P E C  
2201 GAGATCATGA CTCGTGGCA GAGCCATAT CTTGGCATTG AAATGCTGA GATTACAAAC TACCTCATCG GCGGAACCG CCTGAAGCAG CCTCCGGAGT  
748 M E E V Y D L M Y Q C W S A D P K Q R P S F T C L R M E L E N I L  
2301 GCATGGAGGA AGTGTATGAT CTCATGTACC AGTGTGGAG GCGGACCCC AAGCAGGCC CAAGTTTAC GTGTCTCGA ATGGAACCTGG AGAACATTCT  
781 G H L S V L S T S Q D P L Y I N I E R A E O P T E S G S P E L H C  
2401 GGGCCACCTG TCTGTGCTGT CCACCAGCA GGACCCCTTG TACATCAACA TTGAGAGAGC TGAGCAGCCT ACTGAGAGTG GCAGCCCTGA GCTGCACTGT  
814 G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S  
2501 GGAGAGCGAT CCAGCAGCA GGCAGGGGAC GGCAGTGGC TGGGGCAGT AGGTGGCATC CCCAGTACT CTCGGTACAT CTTACAGCCC GGAGGGCTAT  
848 E S P G Q L E Q Q P E S P L N E N Q R L L L L Q Q G L L P H S S C  
2601 CCAGTCAAC AGGCAGCTG GAGCAGCAGC CAGAAAGCCC CCTCAATGAG AACAGAGGC TGTGTGTGCT GCAGCAAGGG CTACTGCCTC ACAGTAGCTG  
881 O  
2701 TTAACCTCA GGCAGAGGAA AGTTGGGGCC CCTGGCTCTG CTGACCGCTG CTAGGCCAG TCTGATCACA GCCCAGCAG CAAGGTATGG  
2801 AGGCTCCTGT GTAGCCCTC CCAAGCTGTG TGGGCGCTGG ACGGACCAA TTGCCCAATC CCAGTTCTTC CTGCAGCCG TCTGGCCAGC CTGGCATCAG  
2901 TTCAGGCCTT GGCTTAGAG AGGTGAGCCA GAGCTGGTTG CCTGAATGCA GGCAGCTGGC AGGAGGGGAG GGTGGCTATG TTTCCATGG TACCATGGGT  
3001 GTGGATGCA GTAAGGGAG GTAGCAACAG CCTGTGGCC CCTACCCTCC TGGCTGAGCT GTCCTACTT TAGTGCATG TTGGAGCCG CTGCAGCCTG  
3101 GAACTACGA CTGCCCCACCA CACTTGGGCC GAATGGCCAG GTTGGCCCT CTTAAGTCAC AAAGAGATGT CCATGTATTG TTCCCTTTTA GGTGATGATT

FIGURE 1B-3

3201 AGGAAGGGAT TGGCACACTT GGTCCCTTAA GCCCTATGGC AGGAATGGT GGGATATTCT CAGGTCTGAA TCCTCATCAT CTTCCTGATT CCCCACCCCTG  
 3301 CAAAGGCCCTG GAACTGGCTG TGGGGCTCTG ACGCATGCTG AAGGACAAAA GGTACAGAG ATCCGACTTC AAAGGCAGG GTCTGAGTCT GGCAGGTGGA  
 3401 GAGGTGCTAA GGGGCTGGCC CAGGAGTCAG GCATTTTCAG ACCCCTCCAA GCTTCTACAG TCTGTCTGAG CATGCTACCA AGCCCCCAGA TACCCCAAAA  
 3501 CTAACAGAGG CAGTTTTGTC TGAGCCCAGC CCTCCCACAT GATGACCCTT AGGTCTACCC TCCTCTCTAA ATGGACATCC TCGTTTGTCC CAAGTCTCCA  
 3601 GAGAGACTAC TGATGGCTGA TGTGGGTAAG AAAAGTTCCA GGAACCAGGG CTGGGGTGGA ACCAGGGCTG GGGTCGAGGC AGGCTCTTGG GCAGGCTCTT  
 3701 GCTGTTAGGA ACATTTCTAA GCTATTAACT TGCTGTTTCA AAACAAATAA AATTGAAACA TAAAGAAATCA AAAAAAAAAA AAAAA

[illegible]

1	GAATTCCTCGA	GTCTGACGTTG	GACTTGAAGG	AATGCCAAGA	GATGCTGCCC
51	CCACCCCCTT	AGGCCCCGAGG	GATCAGGAGC	TATGGGACCA	GAGGCCCTGT
1				MetGlyPro	GluAlaLeuSer
					*****
101	CATCTTTACT	GCTGCTGCTC	TTGGTGGCAA	GTGGAGATGC	TGACATGAAG
8	SerLeuLe	uLeuLeuLeu	LeuValAlaS	erGlyAspAl	aAspMetLys
	*****	*****	*****	*****	
151	GGACATTTTG	ATCCTGCCAA	GTGCCGCTAT	GCCCTGGGCA	TGCAGGACCG
24	GlyHisPheA	spProAlaLy	sCysArgTyr	AlaLeuGlyM	etGlnAspArg
201	GACCATCCCA	GACAGTGACA	TCTCTGCTTC	CAGCTCCTGG	TCAGATTCCA
41	ThrIlePro	AspSerAspI	leSerAlaSe	rSerSerTrp	SerAspSerThr
251	CTGCCGCCCCG	CCACAGCAGG	TTGGAGAGCA	GTGACGGGGA	TGGGGCCTGG
58	AlaAlaAr	gHisSerArg	LeuGluSerS	erAspGlyAs	pGlyAlaTrp
301	TGCCCCGCAG	GGTCGGTGTT	TCCCAAGGAG	GAGGAGTACT	TGCAGGTGGA
74	CysProAlaG	lySerValPh	eProLysGlu	GluGluTyrL	euGlnValAsp
351	TCTACAACGA	CTGCACCTGG	TGGCTCTGGT	GGGCACCCAG	GGACGGCATG
91	LeuGlnArg	LeuHisLeuV	alAlaLeuVa	lGlyThrGln	GlyArgHisAla
401	CCGGGGGGCCT	GGGCAAGGAG	TTCTCCCGGA	GCTACCGGCT	GCGTTACTCC
108	GlyGlyLe	uGlyLysGlu	PheSerArgS	erTyrArgLe	uArgTyrSer
451	CGGGATGGTC	GCCGCTGGAT	GGGCTGGAAG	GACCGCTGGG	GTCAGGAGGT
124	ArgAspGlyA	rgArgTrpMe	tGlyTrpLys	AspArgTrpG	lyGlnGluVal
501	GATCTCAGGC	AATGAGGACC	CTGAGGGAGT	GGTGCTGAAG	GACCTTGGGC
141	IleSerGly	AsnGluAspP	roGluGlyVa	lValLeuLys	AspLeuGlyPro
551	CCCCCATGGT	TGCCCCGACTG	GTTTCGCTTCT	ACCCCCGGGC	TGACCGGGTC
158	ProMetVa	lAlaArgLeu	ValArgPheT	yrProArgAl	aAspArgVal
601	ATGAGCGTCT	GTCTGCGGGT	AGAGCTCTAT	GGCTGCCTCT	GGAGGGATGG
174	MetSerValC	ysLeuArgVa	lGluLeuTyr	GlyCysLeuT	rpArgAspGly
651	ACTCCTGTCT	TACACCGCCC	CTGTGGGGCA	GACAATGTAT	TTATCTGAGG
191	LeuLeuSer	TyrThrAlaP	roValGlyGl	nThrMetTyr	LeuSerGluAla
701	CCGTGTACCT	CAACGACTCC	ACCTATGACG	GACATACCGT	GGGCGGACTG
208	ValTyrLe	uAsnAspSer	ThrTyrAspG	lyHisThrVa	lGlyGlyLeu
751	CAGTATGGGG	GTCTGGGCCA	GCTGGCAGAT	GGTGTGGTGG	GGCTGGATGA
224	GlnTyrGlyG	lyLeuGlyGl	nLeuAlaAsp	GlyValValG	lyLeuAspAsp
801	CTTTAGGAAG	AGTCAGGAGC	TGCGGGTCTG	GCCAGGCTAT	GACTATGTGG
241	PheArgLys	SerGlnGluL	euArgValTr	pProGlyTyr	AspTyrValGly
851	GATGGAGCAA	CCACAGCTTC	TCCAGTGGCT	ATGTGGAGAT	GGAGTTTGAG
258	TrpSerAs	nHisSerPhe	SerSerGlyT	yrValGluMe	tGluPheGlu

Figure 2-2

901 TTTGACCGGC TGAGGGCCTT CCAGGCTATG CAGGTCCACT GTAACAACAT  
274 PheAspArgL euArgAlaPh eGlnAlaMet GlnValHisC ysAsnAsnMet

951 GCACACGCTG GGAGCCCGTC TGCCTGGCGG GGTGGAATGT CGCTTCCGGC  
291 HisThrLeu GlyAlaArgL euProGlyGl yValGluCys ArgPheArgArg

1001 GTGGCCCTGC CATGGCCTGG GAGGGGGAGC CCATGCGCCA CAACCTAGGG  
308 GlyProAl aMetAlaTrp GluGlyGluP roMetArgHi sAsnLeuGly

1051 GGCAACCTGG GGGACCCAG AGCCCGGGCT GTCTCAGTGC CCCTTGGCGG  
324 GlyAsnLeuG lyAspProAr gAlaArgAla ValSerValP roLeuGlyGly

1101 CCGTGTGGCT CGCTTTCTGC AGTGCCGCTT CCTCTTTGCG GGGCCCTGGT  
341 ArgValAla ArgPheLeuG lnCysArgPh eLeuPheAla GlyProTrpLeu

1151 TACTCTTCAG CGAAATCTCC TTCATCTCTG ATGTGGTGAA CAATTCCTCT  
358 LeuPheSe rGluIleSer PheIleSerA spValValAs nAsnSerSer

1201 CCGGCACTGG GAGGCACCTT CCCGCCAGCC CCCTGGTGGC CGCCTGGCCC  
374 ProAlaLeuG lyGlyThrPh eProProAla ProTrpTrpP roProGlyPro

1251 ACCTCCCACC AACTTCAGCA GCTTGGAGCT GGAGCCCAGA GGCCAGCAGC  
391 ProProThr AsnPheSerS erLeuGluLe uGluProArg GlyGlnGlnPro

1301 CCGTGGCCAA GCCCGAGGGG AGCCCGACCG CCATCCTCAT CGGCTGCCTG  
408 ValAlaLy sProGluGly SerProThrA laIleLeuIl eGlyCysLeu

1351 GTGGCCATCA TCCTGCTCCT GCTGCTCATC ATTGCCCTCA TGCTCTGGCG  
424 ValAlaIleI leLeuLeuLe uLeuLeuIle IleAlaLeuM etLeuTrpArg

1401 GCTGCACTGG CGCAGGCTCC TCAGCAAGGC TGAACGGAGG GTGTTGGAAG  
441 LeuHisTrp ArgArgLeuL euSerLysAl aGluArgArg ValLeuGluGlu

1451 AGGAGCTGAC GGTTACCTC TCTGTCCCTG GGGACACTAT CCTCATCAAC  
458 GluLeuTh rValHisLeu SerValProG lyAspThrIl eLeuIleAsn

1501 AACCGCCAG GTCCTAGAGA GCCACCCCG TACCAGGAGC CCCGGCCTCG  
474 AsnArgProG lyProArgGl uProProPro TyrGlnGluP roArgProArg

1551 TGGGAATCCG CCCCCTCCG CTCCCTGTGT CCCCATGGC TCTGCGTTGC  
491 GlyAsnPro ProHisSerA laProCysVa lProAsnGly SerAlaLeuLeu

1601 TGCTCTCCAA TCCAGCCTAC CGCCTCCTTC TGGCCACTTA CGCCCGTCCC  
508 LeuSerAs nProAlaTyr ArgLeuLeuL euAlaThrTy rAlaArgPro

1651 CCTCGAGGCC CGGGCCCCC CACACCCGCC TGGGCCAAAC CCACCAACAC  
524 ProArgGlyP roGlyProPr oThrProAla TrpAlaLysP roThrAsnThr

1701 CCAGGCCTAC AGTGGGGACT ATATGGAGCC TGAGAAGCCA GGCGCCCCGC  
541 GlnAlaTyr SerGlyAspT yrMetGluPr oGluLysPro GlyAlaProLeu

1751 TTCTGCCCCC ACCTCCCCAG AACAGCGTCC CCCATTATGC CGAGGCTGAC  
558 LeuProPr oProProGln AsnSerValP roHisTyrAl aGluAlaAsp

00236939.012599



090701Z - 016920

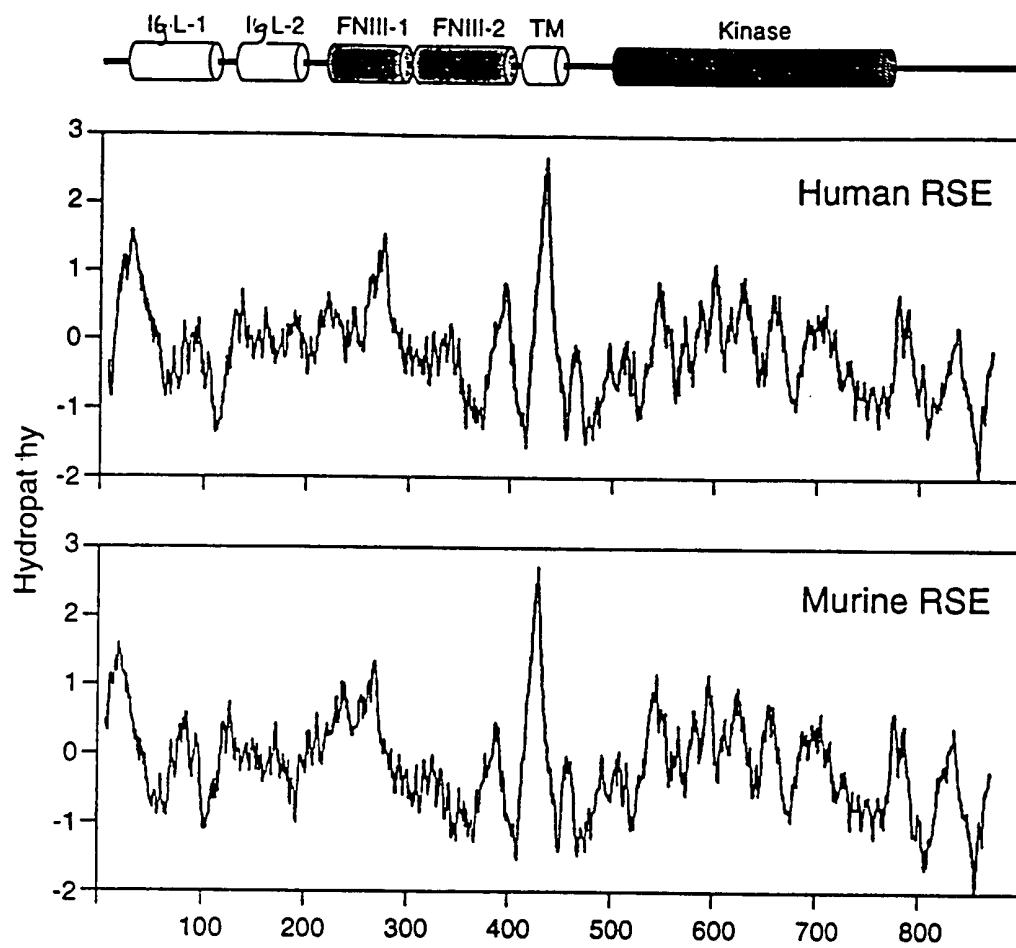
1801	ATTGTTACCC	TGCAGGGCGT	CACCGGGGGC	AACACCTATG	CTGTGCCTGC
574	IleValThrL	euGlnGlyVa	lThrGlyGly	AsnThrTyrA	laValProAla
1851	ACTGCCCCCA	GGGGCAGTCG	GGGATGGGCC	CCCCAGAGTG	GATTTCCCTC
591	LeuProPro	GlyAlaValG	lyAspGlyPr	oProArgVal	AspPheProArg
1901	GATCTCGACT	CCGCTTCAAG	GAGAAGCTTG	GCGAGGGCCA	GTTTGGGGAG
608	SerArgLe	uArgPheLys	GluLysLeuG	lyGluGlyGl	nPheGlyGlu
	<< <		.	.....	.....
1951	GTGCACCTGT	GTGAGGTCGA	CAGCCCTCAA	GATCTGGTCA	GTCTTGATTT
624	ValHisLeuC	ysGluValAs	pSerProGln	AspLeuValS	erLeuAspPhe
2001	CCCCCTTAAT	GTGCGTAAGG	GACACCCTTT	GCTGGTAGCT	GTCAAGATCT
641	ProLeuAsn	ValArgLysG	lyHisProLe	uLeuValAla	ValLysIleLeu
2051	TACGGCCAGA	TGCCACCAAG	AATGCCAGGA	ATGATTTCTT	GAAAGAGGTG
658	ArgProAs	pAlaThrLys	AsnAlaArgA	snAspPheLe	uLysGluVal
2101	AAGATCATGT	CGAGGCTCAA	GGACCCAAAC	ATCATTTCGGC	TGCTGGGCGT
674	LysIleMetS	erArgLeuLy	sAspProAsn	IleIleArgL	euLeuGlyVal
2151	GTGTGTGCAG	GACGACCCCC	TCTGCATGAT	TACTGACTAC	ATGGAGAACG
691	CysValGln	AspAspProL	euCysMetIl	eThrAspTyr	MetGluAsnGly
2201	GCGACCTCAA	CCAGTTCCTC	AGTGCCCACC	AGCTGGAGGA	CAAGGCAGCC
708	AspLeuAs	nGlnPheLeu	SerAlaHisG	lnLeuGluAs	pLysAlaAla
2251	GAGGGGGCCC	CTGGGGACGG	GCAGGCTGCG	CAGGGGGCCA	CCATCAGCTA
724	GluGlyAlaP	roGlyAspGl	yGlnAlaAla	GlnGlyProT	hrIleSerTyr
2301	CCCAATGCTG	CTGCATGTGG	CAGCCCAGAT	CGCCTCCGGC	ATGCGCTATC
741	ProMetLeu	LeuHisValA	laAlaGlnIl	eAlaSerGly	MetArgTyrLeu
2351	TGGCCACACT	CAACTTTGTA	CATCGGGACC	TGGCCACGCG	GAAGTGCCTA
758	AlaThrLe	uAsnPheVal	HisArgAspL	euAlaThrAr	gAsnCysLeu
2401	GTTGGGGAAA	ATTTACCAT	CAAAATCGCA	GACTTTGGCA	TGAGCCGGAA
774	ValGlyGluA	snPheThrIl	eLysIleAla	AspPheGlyM	etSerArgAsn
2451	CCTCTATGCT	GGGGACTATT	ACCGTGTGCA	GGGCCGGGCA	GTGCTGCCCA
791	LeuTyrAla	GlyAspTyrT	yrArgValGl	nGlyArgAla	ValLeuProIle
2501	TCCGCTGGAT	GGCCTGGGAG	TGCATCCTCA	TGGGGAAGTT	CACGACTGCG
808	ArgTrpMe	tAlaTrpGlu	CysIleLeuM	etGlyLysPh	eThrThrAla
2551	AGTGACGTGT	GGGCCTTTGG	TGTGACCCTG	TGGGAGGTGC	TGATGCTCTG
824	SerAspValT	rpAlaPheGl	yValThrLeu	TrpGluValL	euMetLeuCys
2601	TAGGGCCCAG	CCCTTTGGGC	AGCTCACCGA	CGAGCAGGTC	ATCGAGAACG
841	ArgAlaGln	ProPheGlyG	lnLeuThrAs	pGluGlnVal	IleGluAsnAla

# FIGURE 2-4

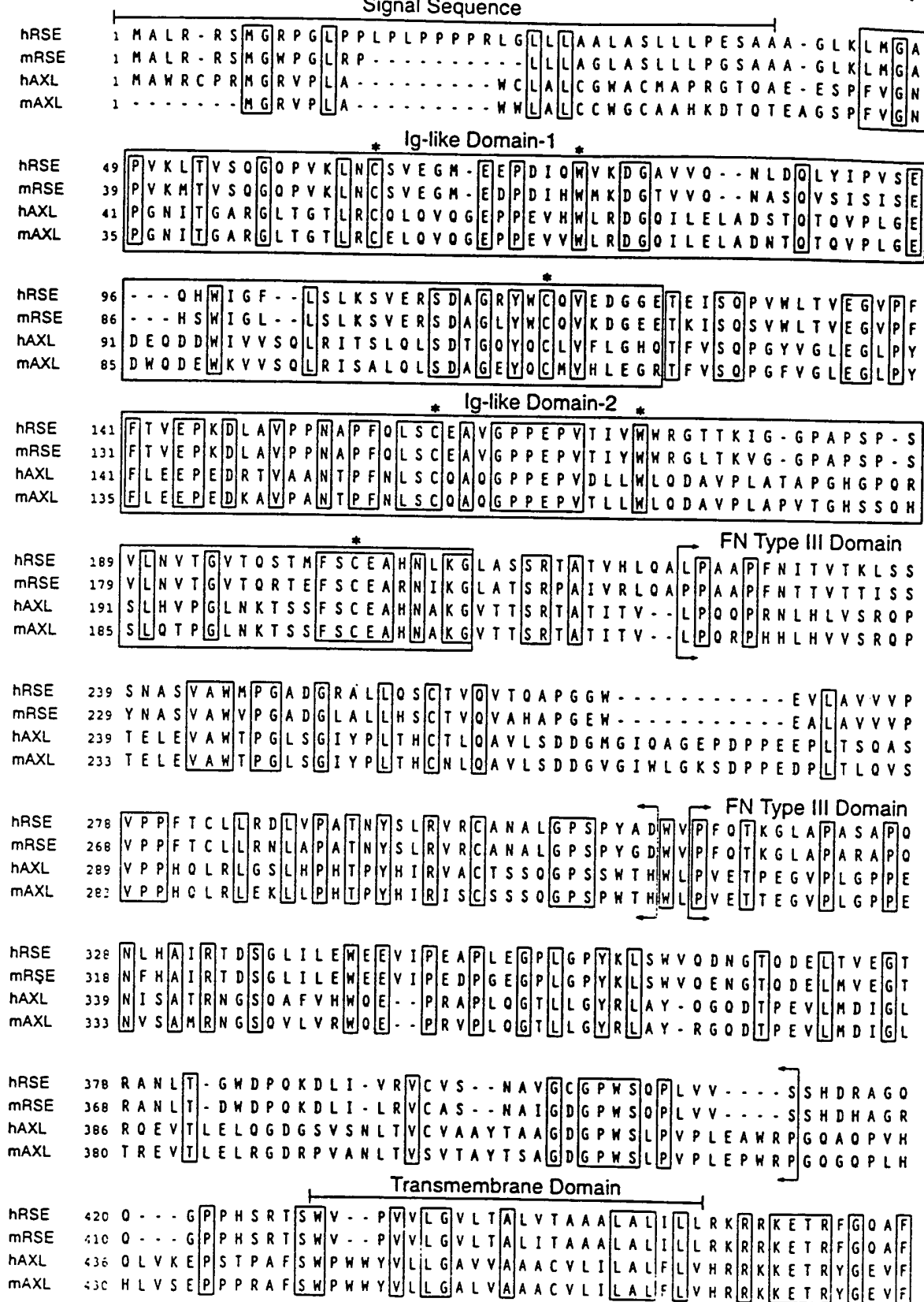
2651 CGGGGGAGTT CTTCCGGGAC CAGGGCCGGC AGGTGTACCT GTCCCGGCCG  
 858 GlyGluPh ePheArgAsp GlnGlyArgG lnValTyrLe uSerArgPro  
 2701 CCTGCCTGCC CGCAGGGCCT ATATGAGCTG ATGCTTCGGT GCTGGAGCCG  
 874 ProAlaCysP roGlnGlyLe uTyrGluLeu MetLeuArgC ysTrpSerArg  
 2751 GGAGTCTGAG CAGCGACCAC CCTTTTCCCA GCTGCATCGG TTCCTGGCAG  
 891 GluSerGlu GlnArgProP roPheSerGl nLeuHisArg PheLeuAlaGlu  
 >>>  
 2801 AGGATGCACT CAACACGGTG TGAATCACAC ATCCAGCTGC CCCTCCCTCA  
 908 AspAlaLe uAsnThrVal  
 2851 GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG GACACAATGG  
 2901 CACCTCTGCC CTTCCCCTCC CGACAGCCCA TCACCTCTAA TAGAGGCAGT  
 2951 GAGACTGCAG AAGCCCCTGT CGCCCACCCA GCTGGTCCTG TGGATGGGAT  
 3001 CCTCTCCACC CTCCTCTAGC CATCCCTTGG GGAAGGGTGG GGAGAAATAT  
 3051 AGGATAGACA CTGGACATGG CCCATTGGAG CACCTGGGCC CCACTGGACA  
 3101 ACACTGATTC CTGGAGAGGT GGCTGCGCCC CCAGCTTCTC TCTCCCTGTC  
 3151 ACACACTGGA CCCCCTGGC TGAGAATCTG GGGGTGAGGA GGACAAGAAG  
 3201 GAGAGGAAAA TGTTTCCTTG TGCCTGCTCC TGTACTTGTC CTCAGCTTGG  
 3251 GCTTCTTCCT CCTCCATCAC CTGAAACACT GGACCTGGGG GTAGCCCCGC  
 3301 CCCAGCCCTC AGTCACCCCC ACTTCCCACC TGCAGTCTTG TAGCTAGAAC  
 3351 TTCTCTAAGC CTATACGTTT CTGTGGAGTA AATATTGGGA TTGGGGGGAA  
 3401 AGAGGGAGCA ACGGCCATA GCCTTGGGGT TGGACATCTC TAGTGTAGCT  
 3451 GCCACATTGA TTTTCTATA ATCACTTGGG GTTGTACAT TTTTGGGGGG  
 3501 AGAGACACAG ATTTTACAC TAATATATGG ACCTAGCTTG AGGCAATTTT  
 3551 AATCCCCTGC ACTAGGCAGG TAATAATAAA GGTGAGTTT TCCACAAAAA  
 3601 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

09236939.012599

FIGURE 3



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[illegible]

**09-0367**

465 DSVMAARGEPAVHFRAARSFNRERPERIEATLDSLGISDELKEKLEEDVLIP  
mRSE 455 DSVMAARGEPAVHFRAARSFNRERPERIEATLDSLGISDELKEKLEEDVLIP  
hAXL 486 EPTVERGE LVVRYRVRKSYSR - - - RTTEATLNSLGISDELKEKLRDVMVD  
mAXL 480 EPTVERGE LVVRYRVRKSYSR - - - RTTEATLNSLGISDELKEKLRDVMVD

I Tyrosine Kinase Domain II

hRSE 515 E Q O F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E  
mRSE 505 E Q O F T L G R M L G K G E F G S V R E A Q L K Q E D G S F V K V A V K M L K A D I I A S S D I E E  
hAXL 533 R H K V A L G K T L G E G E F G A V M E G Q L N O D D - S I L K V A V K T M K I A I C T R S E L E D  
mAXL 527 R H K V A L G K T L G E G E F G A V M E G Q L N O D D - S I L K V A V K T M K I A I C T R S E L E D

III IV V

hRSE 565 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F  
mRSE 555 F L R E A A C M K E F D H P H V A K L V G V S L R S R A K G R L P I P M V I L P F M K H G D L H A F  
hAXL 582 F L S E A V C M K E F D H P N V M R L I G V C F O G S E R E S F P A P V V I L P F M K H G D L H S F  
mAXL 576 F L S E A V C M K E F D H P N V M R L I G V C F O G S D R E G F P E P V V I L P F M K H G D L H S F

VIa VIb

hRSE 615 L L A S R I G E N P F N L P L Q T L I R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A  
mRSE 605 L L A S R I G E N P F N L P L Q T L V R F M V D I A C G M E Y L S S R N F I H R D L A A R N C M L A  
hAXL 632 L L Y S R L G D Q P V Y L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N  
mAXL 626 L L Y S R L G D Q P V F L P T Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M L N

VII VIII

hRSE 665 E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L L P V K W L A L E S L A D N L Y T V Q S D  
mRSE 655 E D M T V C V A D F G L S R K I Y S G D Y Y R Q G C A S K L L P V K W L A L E S L A D N L Y T V H S D  
hAXL 682 E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K W I A I E S L A D R V Y T S K S D  
mAXL 676 E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V K W I A I E S L A D R V Y T S K S D

IX X

hRSE 715 V W A F G V T M W E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E D V Y D L  
mRSE 705 V W A F G V T M W E I M T R G Q T P Y A G I E N A E I Y N Y L I G G N R L K O P P E C M E E V Y D L  
hAXL 732 V W S F G V T M W E I A T R G Q T P Y P G V E N S E I Y D Y L R Q G N R L K O P A D C L D G L Y A L  
mAXL 726 V W S F G V T M W E I A T R G Q T P Y P G V E N S E I Y D Y L R Q G N R L K O P V D F L D G L Y S L

XII

hRSE 765 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G Q L S V L S A S O D P L Y I N I E R A E E P T  
mRSE 755 M Y Q C W S A D P K Q R P S F T C L R M E L E N I L G H L S V L S T S O D P L Y I N I E R A E O P T  
hAXL 782 M S R C W E L N P Q D R P S F T E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G G Y P  
mAXL 776 M S R C W E L N P R D R P S F A E L R E D L E N T L K A L P P A O E P D E I L Y V N M D E G G S H L

hRSE 815 A G G S L E L P G R D O P Y S G A G D G S G M G A V G G T P S D C R Y I L T P G G L A E O P G O A E  
mRSE 805 E S G S P E L H C G E R S S S E A G D G S G V G A V G G I P S D S R Y I F S P G G L S E S P G O L E  
hAXL 832 E P P G A A G G A D P P T O P D P K D S C S C L T A A E V H P A G R Y V L C P S T - T P S P A Q P A  
mAXL 826 E P R G A A G G A D P P T O P D P K D S C S C L T A A D V H S A G R Y V L C P S T - A P G P T L S A

hRSE 865 H O P E S P L N E T Q R L L L L L O O G L L P H S S C  
mRSE 855 O O P E S P L N E N Q R L L L L L O O G L L P H S S C  
hAXL 881 - D R G S P A A P G Q - - - - - E D G A - - - - -  
mAXL 875 - D R G C P A P P G Q - - - - - E D G A - - - - -

FIGURE 5

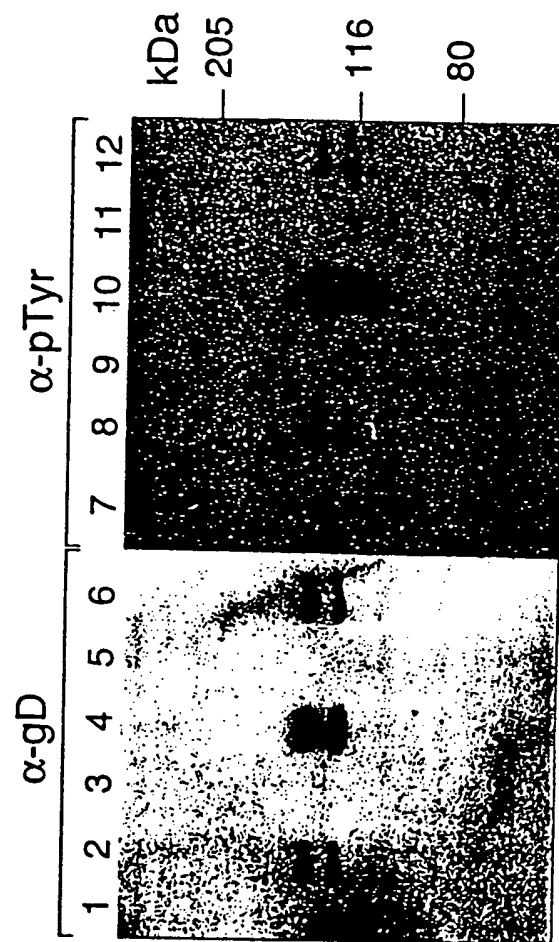
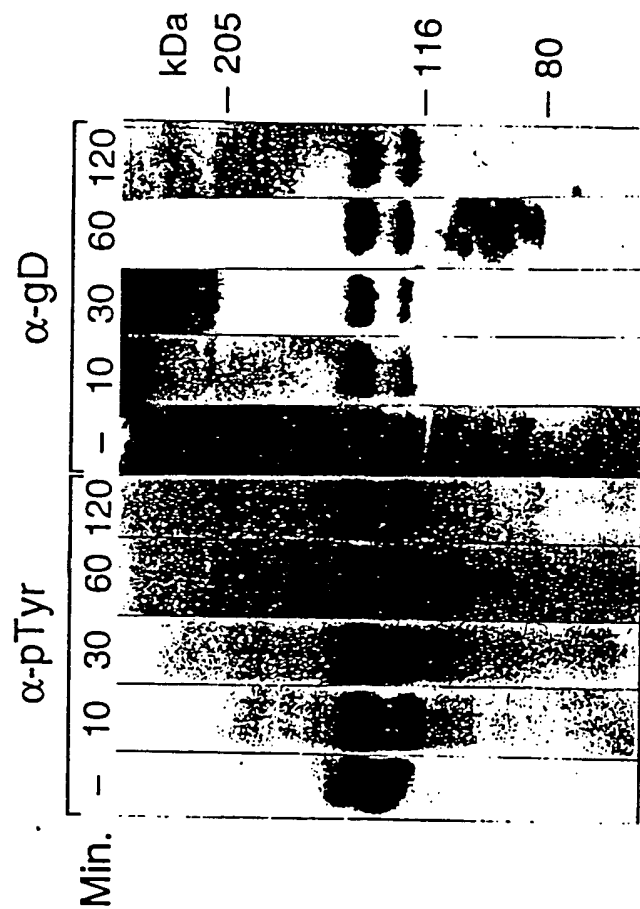


FIGURE 6



655270" 6E69E260

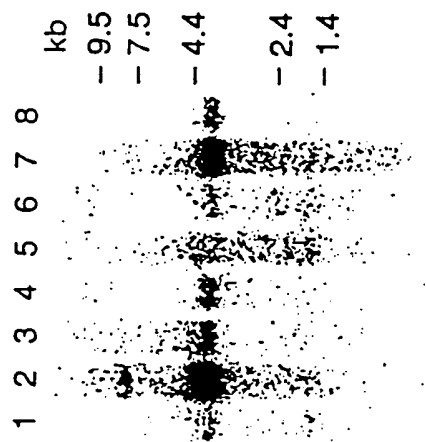


FIGURE 7A



FIGURE 7B



060920Z JUL 78

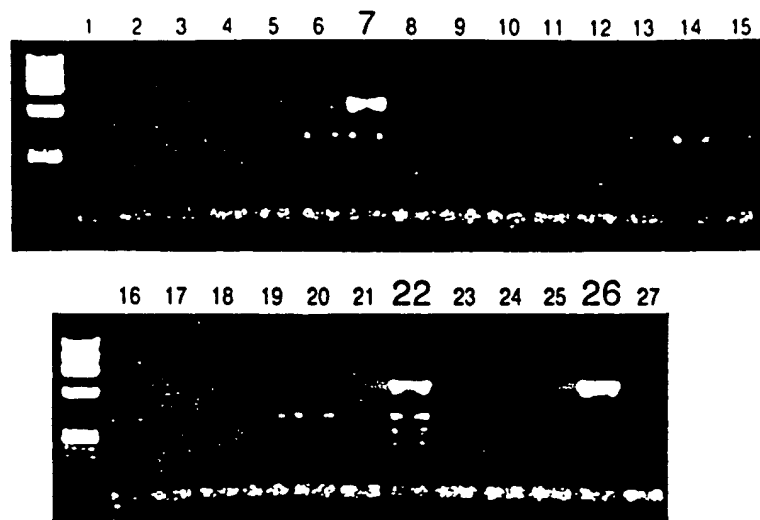


FIGURE 8B

CHROMOSOME CONTENT OF SOMATIC CELL HYBRID PANEL

LANE #	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
CELL LINE	212	324	423	507	683	734	750	716	803	811	852	860	862	867	904	905	937	940	967	968	983	1006	1049	1079	1099
1															*		*								*
2											*														
3			*	*								*												*	
4									*													*			
5	*			*	*	*	*	*	*			*	*	*	*	*	*	*	*	*	*	*	*	*	*
6								*				*			*	*									
7								*														*			
8									*	*							*		*			*			
9						*							*						*						
10											*										*				
11								*															*		
12			*	*				*							*										
13							*	*						*					*		*				*
14			*	*		*	*							*	*	*									
15					*																*				
16															*				*					*	
17									*								*								
18		*			*					*				*											
19				*		*	*				*	*		*				*				*			
20				*			*											*							
21				*			*					*		*			*								
22			*	*				*												*					*
23								*							*					*					
24																*									
25	*		*			*				*					*						*				

FIGURE 9.

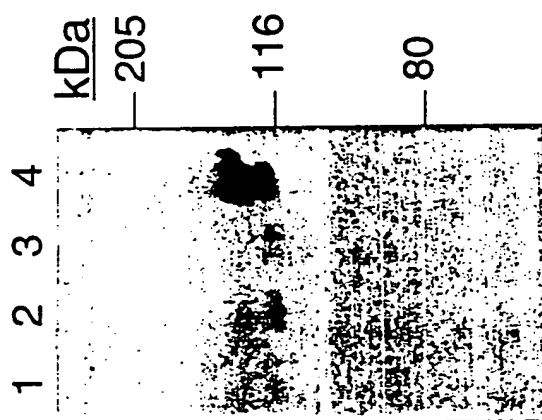
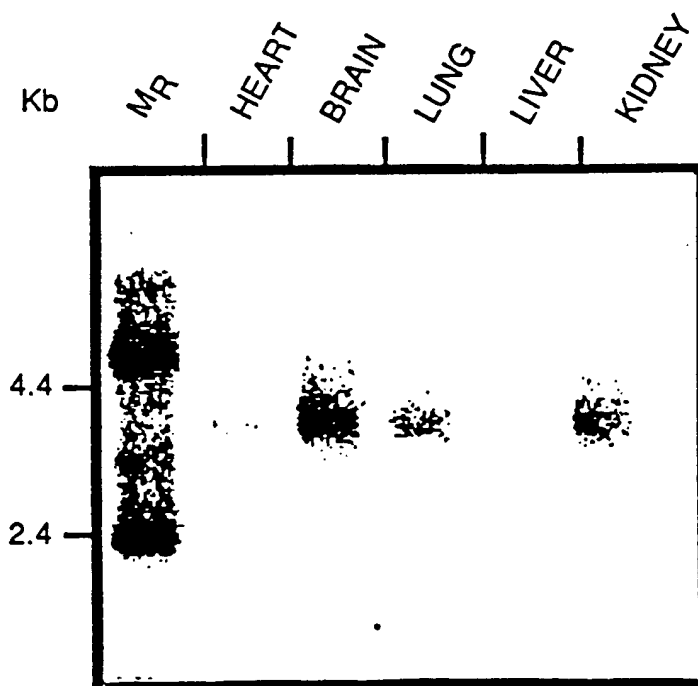


FIGURE 10A.



FIGURE 10 B.



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665210" 66692260

FIGURE 11A

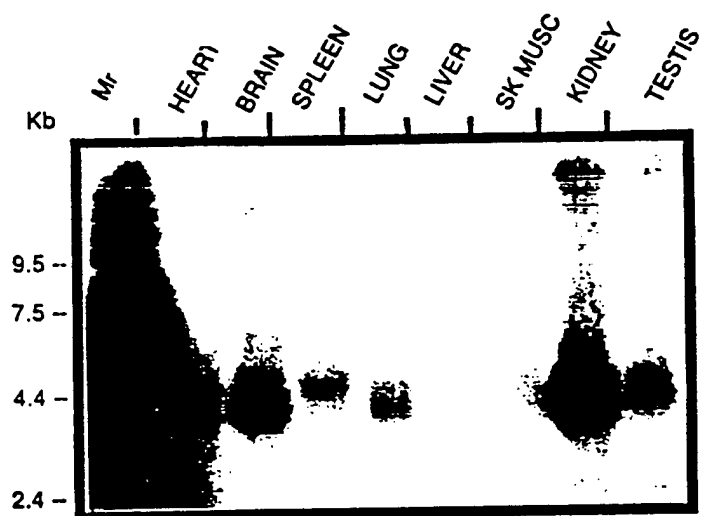


FIGURE 11B

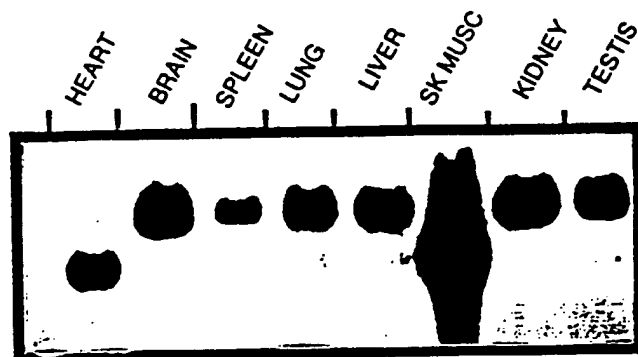


FIGURE 12A  
HUMAN -ve STRAND



FIGURE 12B  
MOUSE -ve STRAND

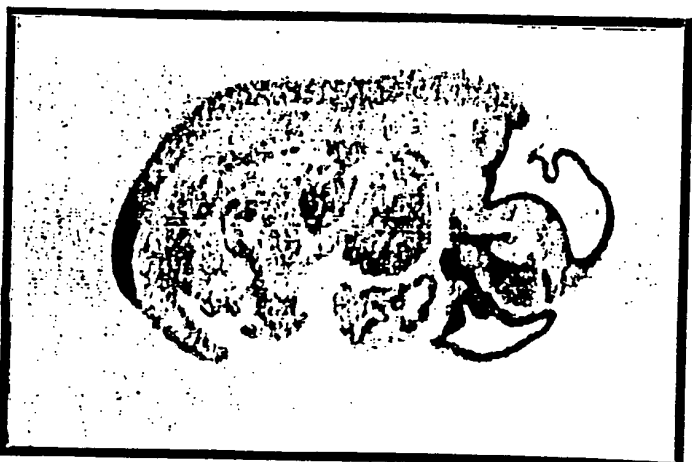
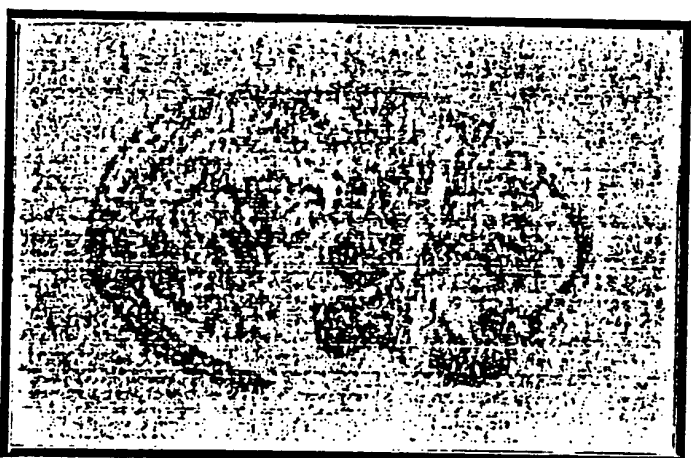


FIGURE 12C  
MOUSE +ve STRAND



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